

**S4 Table. Host candidate genes in the mapped QTL for lesion size (GN trait ID: 17525) on mouse Chr 18 between 49.5 and 56.3Mb**

| Gene symbol | Chr 18 (Mb) | Gene description                                 | GO biological process   | nsSNPs (B6 vs. D2) | Indels in BXD | Score (0-4) |
|-------------|-------------|--|---|--------------------|---------------|-------------|
| Hsd17b4     | 50.29       | Hydroxysteroid (17-beta) dehydrogenase 4         | Very-long-chain fatty acid metabolic process, oxidation reduction   | 30                 | 2             | 4           |
| Snx24       | 53.41       | Sorting nexin 24                                 | Protein transport, cell communication   | 27                 | 10            | 4           |
| Zfp474      | 52.78       | Zinc finger protein 474                          | Biological process  | 10                 | 5             | 4           |
| Srfbp1      | 52.63       | Serum response factor binding protein 1          | Regulation of transcription   | 30                 | 16            | 4           |
| Dmx1l       | 49.99       | Dmx-like 1                                       | Biological process  | 6                  | 2             | 4           |
| Snaip       | 52.93       | Synuclein, alpha interacting protein (synphilin) | Regulation of neurotransmitter secretion  | 3                  | 8             | 3           |
| Tnfaip8     | 50.21       | Tumor necrosis factor, alpha-induced protein 8   | Apoptosis   | 2                  | 13            | 3           |
| Ftmt        | 52.49       | Ferritin mitochondrial                           | Oxidation reduction, cellular iron ion homeostasis  | 12                 | 0             | 2           |
| Lox         | 52.68       | Lysyl oxidase                                    | Oxidation reduction, collagen fibril organization, wound healing  | 4                  | 0             | 2           |
| Prdm6       | 53.62       | PR domain containing 6                           | Neurogenesis, negative regulation of transcription, negative regulation of smooth muscle cell differentiation | 1                  | 2             | 2           |
| Zfp608      | 55.05       | Zinc finger protein 608                          | Biological process  | 1                  | 0             | 2           |
| Prr16       | 51.28       | Proline rich 16                                  | Biological  | 0                  | 4             | 2           |

|               |       |   |  |   |   |   |
|---------------|-------|---|--|---|---|---|
|               |       |   | process  |   |   |   |
| Dtwd2         | 49.86 | DTW domain containing 2                       | Biological process   | 0 | 1 | 2 |
| Csnk1g3       | 54.02 | Casein kinase 1, gamma 3                      | Wnt receptor signaling pathway, protein amino acid phosphorylation | 0 | 0 | 1 |
| Ppic          | 53.57 | Peptidylprolyl isomerase C                    | Protein folding  | 0 | 0 | 1 |
| Snx2          | 53.34 | Sorting nexin 2                               | Protein transport, cell communication                              | 0 | 0 | 1 |
| 1700034E13Rik | 52.81 | RIKEN cDNA 1700034E13 gene                    | Biological process   | 0 | 3 | 1 |
| Gykl1         | 52.85 | Glycerol kinase-like 1                        | Spermatogenesis  | 0 | 0 | 0 |
| Hdhd1a        | 50.73 | Haloacid dehalogenase-like hydrolase domain   | Metabolic process  | 0 | 0 | 0 |
| Cep120        | 53.84 | Centrosomal protein 120                       | Interkinetic nuclear migration, cell proliferation                 | 0 | 0 | 0 |
| Fam170a       | 50.44 | Family with sequence similarity 170, member A | Biological process   | 0 | 0 | 0 |
| Thap11        | 52.62 | THAP domain containing 11                     |  | 0 | 0 | 0 |